

Figure 1A

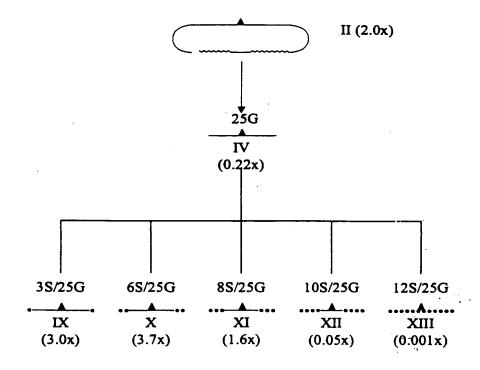
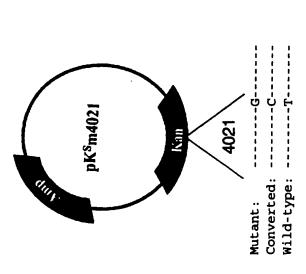


Figure 1B

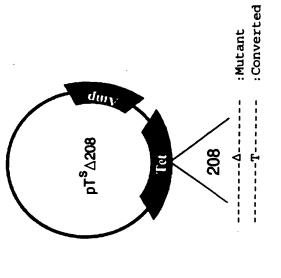
## DOBLESZE GECZCI

# Plasmids, DNA targets and chimeric oligonucleotides



## KanGG





### Tet∆208T

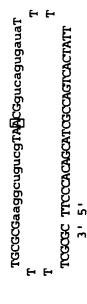


Figure 1C

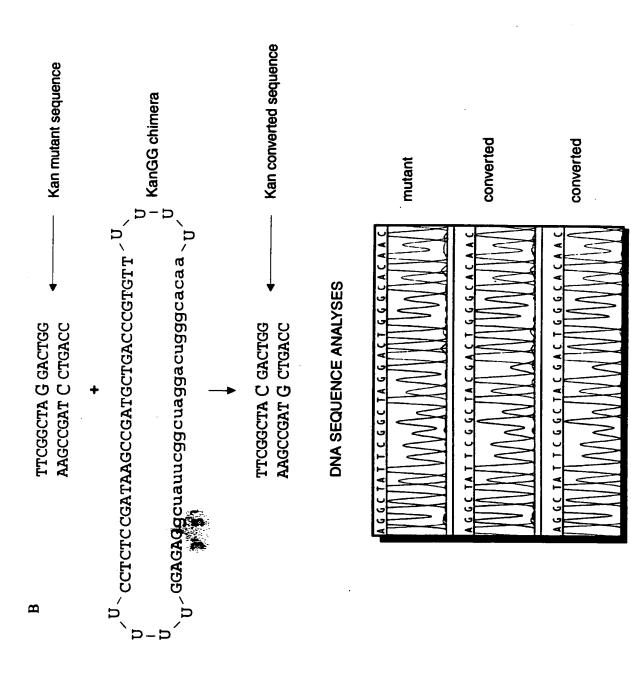


Figure 1D

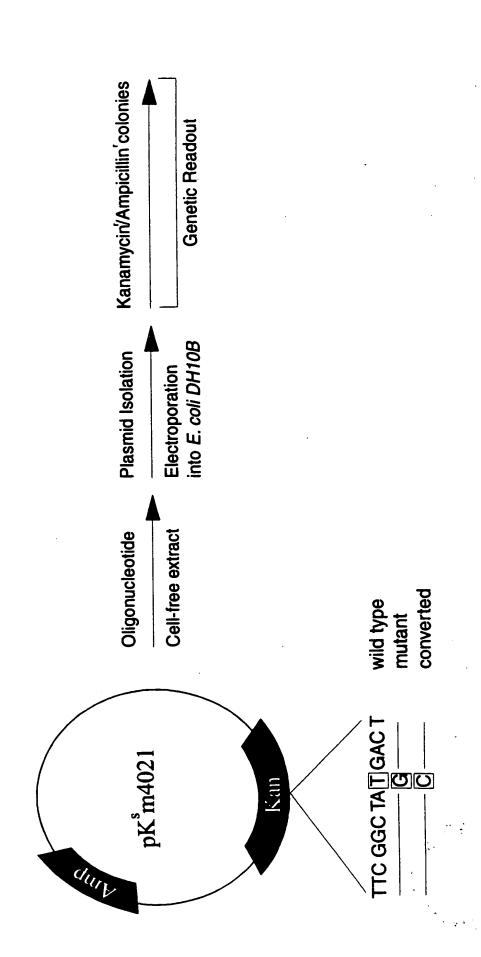
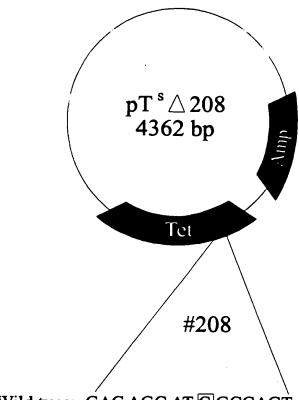


Figure 2



Wild type: GAC AGC AT CGCCAGT Mutant: GAC AGC AT - GCCAGT Converted: GAC AGC AT TGCCAGT

#### Sequence analysis of Tet<sup>r</sup> plasmid △208

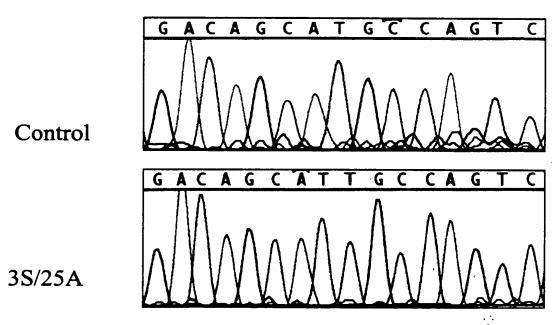
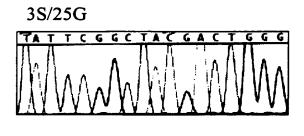
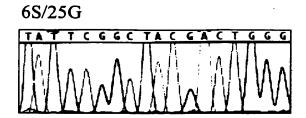


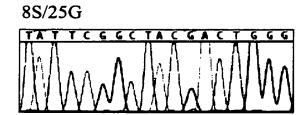
Figure 3

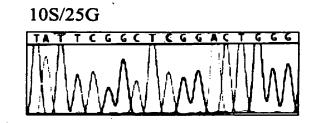
#### DNA sequence analysis of Kan<sup>r</sup> plasmids

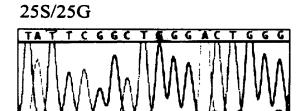
Target codon distr	ibution				
oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)		+			
2) 6S/25G (20)		+	****		
3) 8S/25G (20)		+	*****		
4) 10S/25G (18)		+		+(2)	+(2)
5) 25S/25G (4)			+(2)	+(2)	











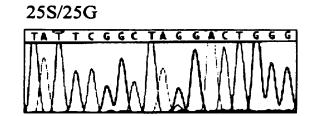


Figure 4

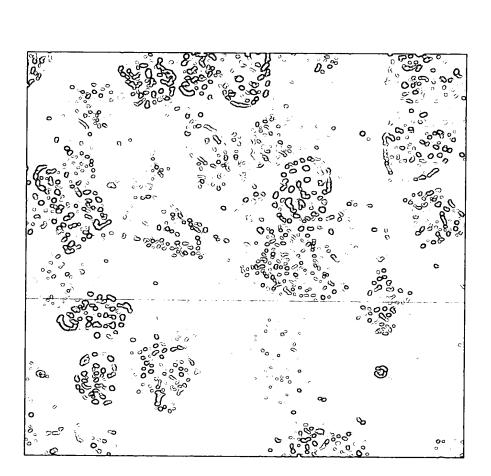


Figure 5

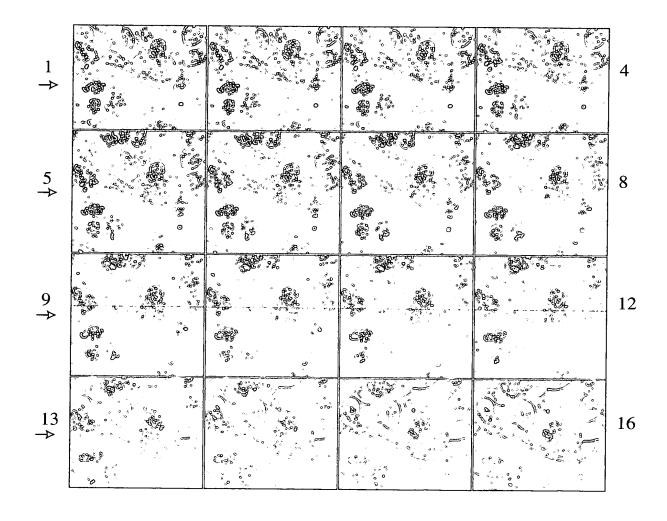


Figure 6

# DOWLOOD ... OBOVEL

Sequence of normal allele: GTGGATATGTCCT Target/existing mutant: GTGGATAATGTCCT Desired alteration:

Figure 7A

pAURHYG(x)EGFP

Sequence of normal allele: GTGGATATGTCCT Target/existing mutant: GTGGATAGGTCCT Desired alteration: GTGGATACGTCCT

nutation at position 137 of the hyg coding region Figure 7B

HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HygE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3'

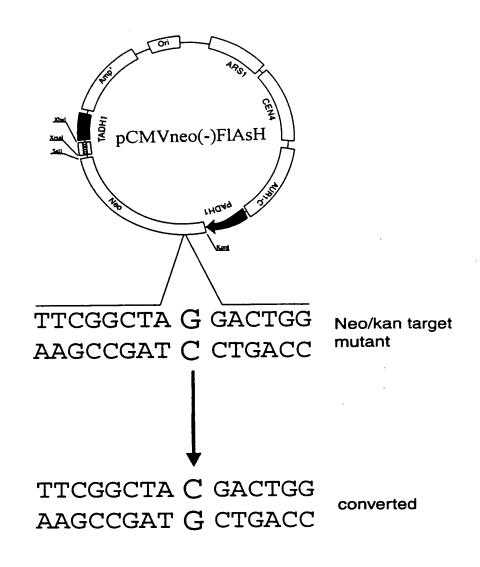
HygE3T/74 $\alpha$ : 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC ACG AG-3'

#### HyqGG/Rev:

T
/ \
T ACATCCTCCCGCACCTATGCAGGACGCCCAT T
T TGTAGGagggcguggaTAGGTccugcgggua T
\ / / \
T 3' 5' T

Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG A-3'

Figure 8



#### FUSION GENE FOR LIGAND BINDING

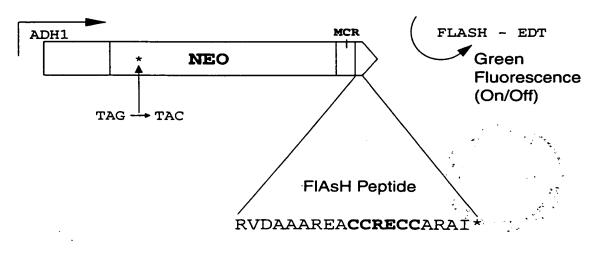


Figure 9

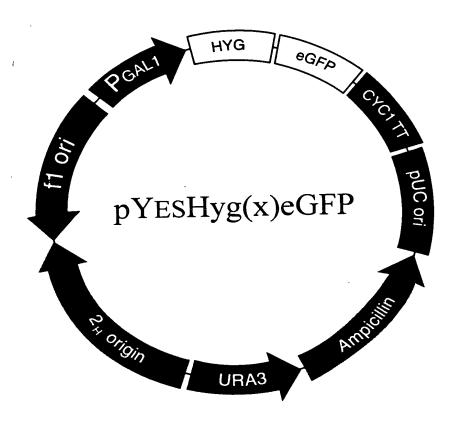


Figure 10